Resource Summary Report

Generated by RRID on Aug 22, 2026

pwtCas9-bacteria

RRID:Addgene_44250
Type: Plasmid

Proper Citation

RRID:Addgene_44250

Plasmid Information

URL: http://www.addgene.org/44250

Proper Citation: RRID:Addgene_44250

Insert Name: wild-type Cas9

Organism: S .pyogenes

Bacterial Resistance: Ampicillin

Defining Citation: PMID:23452860

Vector Backbone Description: Vector Backbone:pUC19; Vector Types:Bacterial Expression, CRISPR; Bacterial Resistance:Ampicillin

Plasmid Name: pwtCas9-bacteria

Record Creation Time: 20220422T222229+0000

Record Last Update: 20260815T081513+0000

Ratings and Alerts

No rating or validation information has been found for pwtCas9-bacteria.

No alerts have been found for pwtCas9-bacteria.

Data and Source Information

Source: Addgene

Usage and Citation Metrics

We found 17 mentions in open access literature.

Listed below are recent publications. The full list is available at RRID .

Herring-Nicholas A, et al. (2024) Selection of extended CRISPR RNAs with enhanced targeting and specificity. Communications biology, 7(1), 86.

Burian J, et al. (2023) High-throughput retrieval of target sequences from complex clone libraries using CRISPRi. Nature biotechnology, 41(5), 626.

Zhu Y, et al. (2023) Inhibition of CXorf56 promotes PARP inhibitor-induced cytotoxicity in triple-negative breast cancer. NPJ breast cancer, 9(1), 34.

Herring-Nicholas A, et al. (2023) Selection of Extended CRISPR RNAs with Enhanced Targeting and Specificity. bioRxiv : the preprint server for biology.

Huszár K, et al. (2023) Position-dependent sequence motif preferences of SpCas9 are largely determined by scaffold-complementary spacer motifs. Nucleic acids research.

Tsuji A, et al. (2022) Establishment of genetic tools for genomic DNA engineering of Halomonas sp. KM-1, a bacterium with potential for biochemical production. Microbial cell factories, 21(1), 122.

Liu X, et al. (2022) The Involvement of Thiamine Uptake in the Virulence of Edwardsiella piscicida. Pathogens (Basel, Switzerland), 11(4).

Contreras-Llano LE, et al. (2020) Holistic engineering of cell-free systems through proteome-reprogramming synthetic circuits. Nature communications, 11(1), 3138.

Hamamoto K, et al. (2020) Characterization of blaCTX-M-14 transposition from plasmid to chromosome in Escherichia coli experimental strain. International journal of medical microbiology : IJMM, 310(2), 151395.

Audibert S, et al. (2020) Addressing the role of centromere sites in activation of ParB proteins for partition complex assembly. PloS one, 15(5), e0226472.

Dong H, et al. (2019) Exploiting a conjugative CRISPR/Cas9 system to eliminate plasmid harbouring the mcr-1 gene from Escherichia coli. International journal of antimicrobial agents, 53(1), 1.

Mehrer CR, et al. (2018) Anaerobic production of medium-chain fatty alcohols via a ?-reduction pathway. Metabolic engineering, 48, 63.

Zheng K, et al. (2018) Highly efficient base editing in bacteria using a Cas9-cytidine deaminase fusion. Communications biology, 1, 32.

Liu F, et al. (2018) Capping-RACE: a simple, accurate, and sensitive 5' RACE method for use in prokaryotes. Nucleic acids research, 46(21), e129.

Zhang K, et al. (2016) Multigene disruption in undomesticated Bacillus subtilis ATCC 6051a using the CRISPR/Cas9 system. Scientific reports, 6, 27943.

Su T, et al. (2016) A CRISPR-Cas9 Assisted Non-Homologous End-Joining Strategy for One-step Engineering of Bacterial Genome. Scientific reports, 6, 37895.

Briner AE, et al. (2014) Guide RNA functional modules direct Cas9 activity and orthogonality. Molecular cell, 56(2), 333.